

IN THE CLAIMS:

Please amend the claims as follows:

Claims 1-31 (Cancelled)

32. (New) An isolated and purified nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 13.

33. (New) The nucleic acid molecule according to claim 1 wherein the molecules are from about 10 to 20 nucleotides in length.

34. (New) A composition consisting essentially of an isolated nucleic acid molecule consisting essentially of the nucleotide sequence of SEQ ID NO: 13.

35. (New) The composition of claim 3, further comprising one or more nucleic acid molecules comprising the nucleotide sequence of any one of SEQ ID NO: 1 to 12 or 14 to 68.

36. (New) The composition according to claim 3 or 4 wherein the molecules are between about 10 and 20 nucleotides in length.

37. (New) A primer comprising a nucleotide sequence corresponding to the nucleotide sequence from position 586 to 606 or position 791 to 810 of SEQ ID NO: 13.

38. (New) A composition comprising the primer according to claim 6.

39. (New) A composition comprising the primer according to claim 6, and further comprising one or more primers comprising a nucleotide sequence corresponding to any of

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primer 1 or primer 2 in the table below:

SEQ ID NO:	H specificity	Positions of primer 1	Positions of primer 2
66	1	892-909	1172-1189
67	2	568-587	1039-1056
6, 17, 42	4	466-483	628-648
7	5	697-714	877-897
8	6	565-585	799-816
9	7	553-570	1483-1500
11	9	616-633	838-855
12 (49)	10	559-579	697-717
14	12	892-909	1172-1189
15	14	586-606	793-813
16	15	640-660	817-834
68	16	649-666	925-942
18	18	589-606	802-819
17	19	607-624	538-855
20	20	574-591	760-780
21, 46	21	676-693	862-879
22	23	637-654	1336-1353
23	24	496-515	772-792
25	26	553-570	772-789
26	27	685-702	799-819
27	28	592-609	778-798
28	29	538-555	757-774
29	30	814-831	943-962
30	31	571-588	790-807
31	32	514-831	1057-1074
32	33	553-570	718-735
33	34	568-585	796-816
36, 53	38	553-573	709-729
37	39	556-573	718-735
39	41	598-615	784-801

<u>40</u>	<u>42</u>	<u>547-567</u>	<u>715-735</u>
<u>41</u>	<u>43</u>	<u>580-597</u>	<u>844-861</u>
<u>43</u>	<u>45</u>	<u>640-657</u>	<u>943-963</u>
<u>44</u>	<u>46</u>	<u>565-582</u>	<u>781-801</u>
<u>48</u>	<u>49</u>	<u>589-609</u>	<u>754-771</u>
<u>50</u>	<u>51</u>	<u>565-582</u>	<u>1042-1059</u>
<u>51</u>	<u>52</u>	<u>598-615</u>	<u>829-846</u>
<u>54</u>	<u>56</u>	<u>697-714</u>	<u>877-897</u>
<u>10 and 38</u>		<u>562-579</u>	<u>1045-1062</u>
<u>24</u>		<u>529-549</u>	<u>703-723</u>
<u>34</u>		<u>769-789</u>	<u>1045-1065</u>
<u>35</u>		<u>520-537</u>	<u>715-735</u>
<u>47</u>		<u>568-585</u>	<u>835-852</u>
<u>52</u>		<u>988-1008</u>	<u>1344-1364</u>

40. (New) A method of detecting the H serotype of *E. coli* in a sample, the method comprising the following steps:

(a) contacting a gene of an *E. coli* in the sample with a nucleic acid molecule according to claim 1, in conditions sufficient to allow the nucleic acid molecule to hybridise to a nucleic acid molecule having a complementary nucleic acid sequence; and

(b) detecting whether the nucleic acid molecule is hybridised to the gene, to detect the H serotype of the *E. coli* in the sample.

41. (New) A method of detecting the H serotype of *E. coli* in a sample, the method comprising the following steps:

(a) contacting a gene of an *E. coli* in the sample with a nucleic acid molecule according to claim 1 and one or more nucleic acid molecules comprising a nucleotide sequence of any one of SEQ ID NO: 1 to 12 or 14 to 44 or 46 to 55 or 57 to 68 or a part thereof, in conditions sufficient to allow at least one of the nucleic acid molecules to hybridise to a nucleic acid molecule having a complementary nucleic acid sequence; and

(b) detecting whether one or more of the at least one nucleic acid molecules is hybridised to the gene, to detect the H serotype of the *E. coli* in the sample.

42. (New) A method according to claim 9 or 10 wherein the hybridised nucleic acid molecules are detected by Southern Blot analysis.

43. (New) A method of detecting the H serotype of *E. coli* in a sample, the method comprising the following steps:

(a) contacting a gene of an *E. coli* in the sample with a pair of nucleic acid molecules according to claim 1, in conditions sufficient to allow the pair of nucleic acid molecules to hybridise to a nucleic acid molecule with a complementary nucleic acid sequence; and

(b) detecting whether the pair of nucleic acid molecules is hybridised to the gene, to detect the H serotype of the *E. coli* in the sample.

44. (New) A method of detecting the H serotype of *E. coli* in a sample, the method comprising the following steps:

(a) contacting a gene of an *E. coli* in the sample with a pair of nucleic acid molecules according to claim 1 and one or more pairs of nucleic acid molecules comprising a nucleic acid sequence of all or part of any one of SEQ ID NO: 1 to 12 or 14 to 44 or 46 to 55 or 57 to 68 or a part thereof, in conditions sufficient to allow at least one pair of nucleic acid molecules to hybridise to a nucleic acid molecule with a complementary nucleic acid sequence; and

(b) detecting whether one or more of the at least one pairs of nucleic acid molecules is hybridised to the gene, to detect the H serotype of the *E. coli* in the sample.

45. (New) A method according to claim 12 or 13 wherein the hybridised pair of nucleic acid molecules are detected by the polymerase chain reaction.

46. (New) A method for detecting the H and O serotype of *E. coli* sample, the method comprising the following steps:

(a) contacting a gene of the *E. coli* with a nucleic acid molecule selected from the group consisting of:

wbdH (nucleotide position 739 to 1932 of SEQ ID NO:45,
wzx (nucleotide position 8646 to 9911 of SEQ ID NO:45,
wzy (nucleotide position 9901 to 10953 of SEQ ID NO:45,
wbdM (nucleotide position 11821 to 12945 of SEQ ID NO:45,
wbdN (nucleotide position 79 to 861 of SEQ ID NO:56),
wbdO (nucleotide position 2011 to 2757 of SEQ ID NO:56),
wbdP (nucleotide position 5257 to 6471 of SEQ ID NO:56),
wbdR (nucleotide position 13156 to 13821 of SEQ ID NO:56),
wzx (nucleotide position 2744 to 4135 of SEQ ID NO:56) and
wzy (nucleotide position 858 to 2042 of SEQ ID NO:56),

in conditions sufficient to allow the nucleic acid molecule to hybridise to a nucleic acid molecule having a complementary nucleic acid sequence;

(b) contacting a gene of an *E. coli* in the sample with a nucleic acid molecule according to claim 1, in conditions sufficient to allow the nucleic acid molecule to hybridise to a nucleic acid molecule having a complementary nucleic acid sequence; and

(c) detecting whether the nucleic acid molecules are hybridised to the genes, to detect the H and O serotype of the *E. coli* in the sample.

47. (New) A method for detecting the H and O serotype of *E. coli* in a sample, the method comprising the following steps:

(a) contacting a gene of the *E. coli* with a nucleic acid molecule selected from the group consisting of:

wbdH (nucleotide position 739 to 1932 of SEQ ID NO:45,
wzx (nucleotide position 8646 to 9911 of SEQ ID NO:45,
wzy (nucleotide position 9901 to 10953 of SEQ ID NO:45,
wbdM (nucleotide position 11821 to 12945 of SEQ ID NO:45,
wbdN (nucleotide position 79 to 861 of SEQ ID NO:56),

wbdO (nucleotide position 2011 to 2757 of SEQ ID NO:56),
wbdP (nucleotide position 5257 to 6471 of SEQ ID NO:56),
wbdR (nucleotide position 13156 to 13821 of SEQ ID NO:56),
wzx (nucleotide position 2744 to 4135 of SEQ ID NO:56) and
wzy (nucleotide position 858 to 2042 of SEQ ID NO:56),
in conditions sufficient to allow the nucleic acid molecule to hybridise to a nucleic acid molecule having a complementary nucleic acid sequence;

(b) contacting a gene of an *E. coli* in the sample with a nucleic acid molecule according to claim 1, in conditions sufficient to allow the nucleic acid molecule and one or more nucleic acid molecules comprising a nucleotide sequence of any one of SEQ ID NO: 1 to 12 or 14 to 44 or 46 to 55 or 57 to 68 or a part thereof, in conditions sufficient to allow at least one of the nucleic acid molecules to hybridise to a nucleic acid molecule having a complementary nucleic acid sequence; and

(c) detecting whether the nucleic acid molecules are hybridised to the genes, to detect the H and O serotype of the *E. coli* in the sample.

48. (New) A method according to claim 15 or 16 wherein the nucleic acid molecule of step (a) is a forward primer or a reverse primer selected from the group of

Forward primer (base position of SEQ ID NO:1)	Reverse Primer (base position of SEQ ID NO:1)
<u>739-757</u>	<u>1941-1924</u>
<u>925-942</u>	<u>1731-1714</u>
<u>925-942</u>	<u>1347-1330</u>
<u>1165-1182</u>	<u>1731-1714</u>
<u>8646-8663</u>	<u>9908-9891</u>
<u>8906-8923</u>	<u>9468-9451</u>
<u>9150-9167</u>	<u>9754-9737</u>
<u>9976-9996</u>	<u>10827-10807</u>
<u>10113-10130</u>	<u>10484-10467</u>

<u>10931-10949</u>	<u>11824-11796</u>
<u>11821-11844</u>	<u>12945-12924</u>
<u>12042-12059</u>	<u>12447-12430</u>
<u>12258-12275</u>	<u>12698-12681</u>

<u>Forward Primer</u> (base position of SEQ ID NO:2)	<u>Reverse Primer</u> (base position of SEQ ID NO:2)
<u>79-96</u>	<u>861-844</u>
<u>184-201</u>	<u>531-514</u>
<u>310-327</u>	<u>768-751</u>
<u>858-875</u>	<u>2042-2025</u>
<u>1053-1070</u>	<u>1619-1602</u>
<u>1278-1295</u>	<u>1913-1896</u>
<u>2011-2028</u>	<u>2757-2740</u>
<u>2110-2127</u>	<u>2493-2476</u>
<u>2305-2322</u>	<u>2682-2665</u>
<u>2744-2761</u>	<u>4135-4118</u>
<u>2942-2959</u>	<u>3628-3611</u>
<u>5257-5274</u>	<u>6471-6454</u>
<u>5440-5457</u>	<u>5973-5956</u>
<u>5707-5724</u>	<u>6231-6214</u>
<u>13261-13278</u>	<u>13629-13612</u>
<u>13384-13401</u>	<u>13731-13714</u>

49. (New) A method according to claim 15 or 16 wherein the hybridised nucleic acid molecules are detected by Southern Blot analysis.

50. (New) A method for detecting the H and O serotype of *E. coli* in a sample, the method comprising the following steps:

(a) contacting a gene of the *E. coli* with a pair of nucleic acid molecules selected from the group consisting of :

wbdH (nucleotide position 739 to 1932 of SEQ ID NO:45,
wzx (nucleotide position 8646 to 9911 of SEQ ID NO:45,
wzy (nucleotide position 9901 to 10953 of SEQ ID NO:45,
wbdM {nucleotide position 11821 to 12945 of SEQ ID NO:45,
wbdN (nucleotide position 79 to 861 of SEQ ID NO:56),
wbdO (nucleotide position 2011 to 2757 of SEQ ID NO:56),
wbdP (nucleotide position 5257 to 6471 of SEQ ID NO:56),
wbdR (nucleotide position 13156 to 13821 of SEQ ID NO:56),
wzx (nucleotide position 2744 to 4135 of SEQ ID NO:56) and
wxy (nucleotide position 858 to 2042 of SEQ ID NO:56)

in conditions sufficient to allow the pair of nucleic acid molecules to hybridise to a nucleic acid molecule having a complementary nucleic acid sequence;

(b) contacting a gene of an *E. coli* in the sample with a pair of nucleic acid molecules according to claim 1, in conditions sufficient to allow the pair of nucleic acid molecules to hybridise to a nucleic acid molecule having a complementary nucleic acid sequence; and

(c) detecting whether the pairs of nucleic acid molecules are hybridised to the genes, to detect the H and O serotype of the *E. coli* in the sample.

51. (New) A method for detecting the H and O serotype of *E. coli* in a sample, the method comprising the following steps:

(a) contacting a gene of the *E. coli* with a pair of nucleic acid molecules selected from the group consisting of:

wbdH (nucleotide position 739 to 1932 of SEQ ID NO:45,
wzx (nucleotide position 8646 to 9911 of SEQ ID NO:45,
wzy (nucleotide position 9901 to 10953 of SEQ ID NO:45,
wbdM (nucleotide position 11821 to 12945 of SEQ ID NO:45,
wbdN (nucleotide position 79 to 861 of SEQ ID NO:56),
wbdO (nucleotide position 2011 to 2757 of SEQ ID NO:56),

wbdP (nucleotide position 5257 to 6471 of SEQ ID NO:56),
wbdR (nucleotide position 13156 to 13821 of SEQ ID NO:56),
wzx (nucleotide position 2744 to 4135 of SEQ ID NO:56) and
wxy (nucleotide position 858 to 2042 of SEQ ID NO:56)

in conditions sufficient to allow the pair of nucleic acid molecules to hybridise to a nucleic acid molecule having a complementary nucleic acid sequence;

(b) contacting a gene of an *E. coli* in the sample with a pair of nucleic acid molecules according to claim 1 and one or more pairs of nucleic acid molecules comprising a sequence of any one of SEQ ID NO: 1 to 12 or 14 to 44 or 46 to 55 or 57 to 68 or a part thereof, in conditions sufficient to allow at least one pair of nucleic acid molecules to hybridise to a nucleic acid molecule having a complementary nucleic acid sequence; and

(c) detecting whether the pairs of nucleic acid molecules are hybridised to the genes, to detect the H and O serotype of the *E. coli* in the sample.

52. (New) A method according to claim 19 or 20 wherein the nucleic acid molecules of the pair of step (a) are a primer pair comprising a forward primer and a reverse primer selected from

Forward primer (base position of SEQ ID NO:1)	Reverse Primer (base position of SEQ ID NO:1)
<u>739-757</u>	<u>1941-1924</u>
<u>925-942</u>	<u>1731-1714</u>
<u>925-942</u>	<u>1347-1330</u>
<u>1165-1182</u>	<u>1731-1714</u>
<u>8646-8663</u>	<u>9908-9891</u>
<u>8906-8923</u>	<u>9468-9451</u>
<u>9150-9167</u>	<u>9754-9737</u>
<u>9976-9996</u>	<u>10827-10807</u>
<u>10113-10130</u>	<u>10484-10467</u>
<u>10931-10949</u>	<u>11824-11796</u>

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<u>11821-11844</u>	<u>12945-12924</u>
<u>12042-12059</u>	<u>12447-12430</u>
<u>12258-12275</u>	<u>12698-12681</u>

Forward primer (base position of SEQ ID NO:2)	Reverse Primer (base position of SEQ ID NO:2)
<u>79-96</u>	<u>861-844</u>
<u>184-201</u>	<u>531-514</u>
<u>310-327</u>	<u>768-751</u>
<u>858-875</u>	<u>2042-2025</u>
<u>1053-1070</u>	<u>1619-1602</u>
<u>1278-1295</u>	<u>1913-1896</u>
<u>2011-2028</u>	<u>2757-2740</u>
<u>2110-2127</u>	<u>2493-2476</u>
<u>2305-2322</u>	<u>2682-2665</u>
<u>2744-2761</u>	<u>4135-4118</u>
<u>2942-2959</u>	<u>3628-3611</u>
<u>5257-5274</u>	<u>6471-6454</u>
<u>5440-5457</u>	<u>5973-5956</u>
<u>5707-5724</u>	<u>6231-6214</u>
<u>13261-13278</u>	<u>13629-13612</u>
<u>13384-13401</u>	<u>13731-13714</u>

53. (New) A method according to claim 19 or 20 wherein the hybridised pairs of nucleic acid molecules are detected by the polymerase chain reaction.

54. (New) A method for detecting the H and O serotype of *E. coli* in a sample, the method comprising the following steps:

(a) contacting a gene of an *E. coli* in the sample with a nucleic acid molecule according to claim 1, in conditions sufficient to allow the nucleic acid molecule to hybridise to the gene; and

(b) detecting whether the nucleic acid molecule is hybridised to the gene, to detect the H and O serotype of *E. coli* in the sample.

55. (New) A method according to claim 19 wherein the gene of an *E. coli* in the sample is contacted with a nucleic acid molecule according to claim 1, and a nucleic acid molecule comprising the nucleotide sequence of any one of SEQ ID NOS: 9, 55, 57 to 65 of a part thereof.

56. (New) A method according to claim 9 or 10 wherein the sample is selected from the group consisting of a sample derived from food, a sample derived from faeces and a sample derived from a patient or animal.

57. (New) A kit for identifying the H serotype of *E. coli*, the kit comprising a nucleic acid molecule according to claim 1, a primer according to claim 6, or a composition according to claim 3, 4 or 8.

58. (New) A kit for identifying the H and O serotype of *E. coli*, the kit comprising:

(a) a nucleic acid molecule according to claim 1; and

(b) at least one nucleic acid molecule selected from the group consisting of:

mbdH (nucleotide position 739 to 1932 of SEQ ID NO: 45),

wzx (nucleotide position 8646 to 9911 of SEQ ID NO: 45),

wzy (nucleotide position 9901 to 10953 of SEQ ID NO: 45),

wbdM (nucleotide position 11821 to 12945 of SEQ ID NO: 45),

wbdN (nucleotide position 79 to 861 of SEQ ID NO: 56),

wbdO (nucleotide position 2011 to 2757 of SEQ ID NO: 56),

wbdP (nucleotide position 5257 to 6471 of SEQ ID NO: 56),

wbdR (nucleotide position 13156 to 13821 of SEQ ID NO: 56),

wzx (nucleotide position 2744 to 4135 of SEQ ID NO: 56) and

wzy (nucleotide position 858 to 2042 of SEQ ID NO: 56).

59. (New) A kit for identifying the H and O serotype of *E. coli*, the kit comprising:
(a) a nucleic acid molecule according to claim 1 and one or more nucleic acid molecules comprising the nucleotide sequence of any one of SEQ ID NO: 1 to 12 or 14 to 44 or 46 to 55 or 57 to 68 or a part thereof; and

(b) at least one nucleic acid molecule selected from the group consisting of:

wbdH (nucleotide position 739 to 1932 of SEQ ID NO: 45),

wzx (nucleotide position 8646 to 9911 of SEQ ID NO: 45),

wzy (nucleotide position 9901 to 10953 of SEQ ID NO: 45),

wbdM (nucleotide position 11821 to 12945 of SEQ ID NO: 45),

wbdN (nucleotide position 79 to 861 of SEQ ID NO: 56),

wbdO (nucleotide position 2011 to 2757 of SEQ ID NO: 56),

wbdP (nucleotide position 5257 to 6471 of SEQ ID NO: 56),

wbdR (nucleotide position 13156 to 13821 of SEQ ID NO: 56),

wzx (nucleotide position 2744 to 4135 of SEQ ID NO: 56) and

wzy (nucleotide position 858 to 2042 of SEQ ID NO: 56).

60. (New) A kit according to claim 27 or 28 wherein the composition of (b) comprises a forward primer or a reverse primer selected from the group of

Forward primer (base position of SEQ ID NO:1)	Reverse Primer (base position of SEQ ID NO:1)
<u>739-757</u>	<u>1941-1924</u>
<u>925-942</u>	<u>1731-1714</u>
<u>925-942</u>	<u>1347-1330</u>
<u>1165-1182</u>	<u>1731-1714</u>
<u>8646-8663</u>	<u>9908-9891</u>
<u>8906-8923</u>	<u>9468-9451</u>
<u>9150-9167</u>	<u>9754-9737</u>
<u>9976-9996</u>	<u>10827-10807</u>
<u>10113-10130</u>	<u>10484-10467</u>

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<u>10931-10949</u>	<u>11824-11796</u>
<u>11821-11844</u>	<u>12945-12924</u>
<u>12042-12059</u>	<u>12447-12430</u>
<u>12258-12275</u>	<u>12698-12681</u>

<u>Forward primer</u> <u>(base position of SEQ</u> <u>ID NO:2)</u>	<u>Reverse Primer</u> <u>(base position of SEQ</u> <u>ID NO:2)</u>
<u>79-96</u>	<u>861-844</u>
<u>184-201</u>	<u>531-514</u>
<u>310-327</u>	<u>768-751</u>
<u>858-875</u>	<u>2042-2025</u>
<u>1053-1070</u>	<u>1619-1602</u>
<u>1278-1295</u>	<u>1913-1896</u>
<u>2011-2028</u>	<u>2757-2740</u>
<u>2110-2127</u>	<u>2493-2476</u>
<u>2305-2322</u>	<u>2682-2665</u>
<u>2744-2761</u>	<u>4135-4118</u>
<u>2942-2959</u>	<u>3628-3611</u>
<u>5257-5274</u>	<u>6471-6454</u>
<u>5440-5457</u>	<u>5973-5956</u>
<u>5707-5724</u>	<u>6231-6214</u>
<u>13261-13278</u>	<u>13629-13612</u>
<u>13384-13401</u>	<u>13731-13714</u>

primers shown in the Tables above.

61. (New) A kit according to claim 27 or 28 wherein the composition of (a) comprises a forward primer and a reverse primer selected from the group of

Forward primer (base position of SEQ ID N0:1)	Reverse Primer (base position of SEQ ID N0:1)
<u>739-757</u>	<u>1941-1924</u>
<u>925-942</u>	<u>1731-1714</u>
<u>925-942</u>	<u>1347-1330</u>
<u>1165-1182</u>	<u>1731-1714</u>
<u>8646-8663</u>	<u>9908-9891</u>
<u>8906-8923</u>	<u>9468-9451</u>
<u>9150-9167</u>	<u>9754-9737</u>
<u>9976-9996</u>	<u>10827-10807</u>
<u>10113-10130</u>	<u>10484-10467</u>
<u>10931-10949</u>	<u>11824-11796</u>
<u>11821-11844</u>	<u>12945-12924</u>
<u>12042-12059</u>	<u>12447-12430</u>
<u>12258-12275</u>	<u>12698-12681</u>

Forward primer (base position of SEQ ID N0:2)	Reverse Primer (base position of SEQ ID N0:2)
<u>79-96</u>	<u>861-844</u>
<u>184-201</u>	<u>531-514</u>
<u>310-327</u>	<u>768-751</u>
<u>858-875</u>	<u>2042-2025</u>
<u>1053-1070</u>	<u>1619-1602</u>
<u>1278-1295</u>	<u>1913-1896</u>
<u>2011-2028</u>	<u>2757-2740</u>
<u>2110-2127</u>	<u>2493-2476</u>
<u>2305-2322</u>	<u>2682-2665</u>
<u>2744-2761</u>	<u>4135-4118</u>
<u>2942-2959</u>	<u>3628-3611</u>
<u>5257-5274</u>	<u>6471-6454</u>
<u>5440-5457</u>	<u>5973-5956</u>

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<u>5707-5724</u>	<u>6231-6214</u>
<u>13261-13278</u>	<u>13629-13612</u>
<u>13384-13401</u>	<u>13731-13714</u>

forward and reverse primers shown in the Tables above.

62. (New) A method according to claim 12 or 13 wherein the sample is selected from the group consisting of a sample derived from food, a sample derived from faeces and a sample derived from a patient or animal.

63. (New) A method according to claim 15 or 16 wherein the sample is selected from the group consisting of a sample derived from food, a sample derived from faeces and a sample derived from a patient or animal.

64. (New) A method according to claim 19 or 20 wherein the sample is selected from the group consisting of a sample derived from food, a sample derived from faeces and a sample derived from a patient or animal.

65. (New) A method according to claim 23 wherein the sample is selected from the group consisting of a sample derived from food, a sample derived from faeces and a sample derived from a patient or animal.

66. (New) A kit for identifying the H and O serotype of *E. coli*, the kit comprising:
(a) at least one primer according to claim 6 or a composition according to claim 8;
and

(b) at least one nucleic acid molecule selected from the group consisting of:
wbdH (nucleotide position 739 to 1932 of SEQ ID NO: 45),
wzx (nucleotide position 8646 to 9911 of SEQ ID NO: 45),
wzy (nucleotide position 9901 to 10953 of SEQ ID NO: 45),

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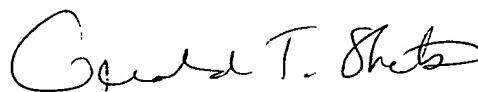
wbdM (nucleotide position 11821 to 12945 of SEQ ID NO: 45),
wbdN (nucleotide position 79 to 861 of SEQ ID NO: 56),
wbdO (nucleotide position 2011 to 2757 of SEQ ID NO: 56),
wbdP (nucleotide position 5257 to 6471 of SEQ ID NO: 56),
wbdR (nucleotide position 13156 to 13821 of SEQ ID NO: 56),
wzx (nucleotide position 2744 to 4135 of SEQ ID NO: 56) and
wzy (nucleotide position 858 to 2042 of SEQ ID NO: 56).

67. (New) A kit for identifying the H serotype of *E. coli*, the kit comprising a nucleic acid molecule according to claim 1 and one or more nucleic acid molecules comprising the nucleotide sequence of any one of SEQ ID NO: 1 to 12, 14 to 44, 46 to 55 or 57 to 68 or a part thereof.

68. (New) A kit comprising a nucleic acid molecule according to claim 1 and one or more nucleic acid molecules comprising the nucleotide sequence of any one of SEQ ID NO: 1 to 12 or 14 to 68 or a part thereof.

Respectfully submitted,

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